

[illegible]

FIG. 1

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F. I. G. I. C.

MATCH WITH FIG. 1D

V C K N K L F P S Q C G A N R E F D E N - C

C T C Q C V C K R T C P R N Q P L N P G K -

C C A C E C T E S P Q K C L L K G K K F H -

C H Q T C S C Y R R P C T N R Q K A C C E P -

C G F S Y S E V C R C V P S Y W Q R P Q -

MATCH WITH FIG. 1E

MS☆

[illegible]

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGACGTTACGGTCTGTCTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
71 AGATGAACCTCATGACTGTACTCTACCCAGAATATTGAAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGGAGCTGGCAACATTAACAGAGAACAGGCCAACCCTCAACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTC
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAAGGAGTTTGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTCTCCGTCTACAGATGTGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C C

FIG. 2A

361 CAATAGTGAGGGCTGCAGTGCATGAACACCAGCAGGCTACCTCAGCAAGACGTTATT
-----+-----+-----+-----+-----+-----+-----+
N S E G L Q C M N T S T S Y L S K T L F
421 TGAATTACAGTGCCCTCTCTCTCAAGGCCCCAACCAGTAACAATCAGTTTGGCCAATCA
-----+-----+-----+-----+-----+-----+-----+
E I T V P L S Q G P K P V T I S F A N H
481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
-----+-----+-----+-----+-----+-----+-----+
T S C R C M S K L D V Y R Q V H S I I R
541 ACGTCCCTGCCAGCACTACCACAGTGTTCAGGCAGCGAACAAGACCTGCCCCACCAA
-----+-----+-----+-----+-----+-----+-----+
R S L P A T L P Q C Q A A N K T C P T N
601 TTACATGTGAATAATCACAATCTGCAGATGCCCTGGCTCAGGAAGATTTTATGTTTCCTC
-----+-----+-----+-----+-----+-----+-----+
Y M W N N H I C R C L A Q E D F M F S S
661 GGATGCTGAGATGACTCAACAGATGGATTCCATGACATCTGTGGAACCAACAAGAGCT
-----+-----+-----+-----+-----+-----+-----+
D A G D D S T D G F H D I C G P N K E L

FIG.2B

1081 TCCTTGTGTCCTTCATATTGCCAAGACCACAATGAGCTAAGATTGTA CTGTTTCCA
-----+-----+-----+-----+-----+
R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
-----+-----+-----+-----+-----+
1201 GAGACCCCTTGTGGCTCCATGCTAACAAGACAAAAGTCTGTCTTCCCTGAACCATGTGGA
-----+-----+-----+-----+-----+
1261 TAACTTTACAGAAATGAGCTGGAGCTCATCTGCCAAAAGCCCTCTGTGTAAGACTGTTT
-----+-----+-----+-----+-----+
1321 CTGCCAATGACCAACAGCCAGATTTTCCCTTGATTTCTTTAAAGAATGACTATA
-----+-----+-----+-----+-----+
1381 TAATTTATTTCCTACTAAAAATATGTCTTCTGCATTCATTTTATAGCAACAATTGCT
-----+-----+-----+-----+-----+
1441 AAAA CTCACTGTGATCAATATTTTATATCATGCCAAAATATGTTTAAATAAATGAAAA
-----+-----+-----+-----+-----+
1501 TTGTATTATAAAAA
-----+-----+-----+-----+-----+

FIG.2D

1

50

Pdgfa .MRTIACLLL LGGCYLAHVL AEEAEIPREV IERLARSQH SIRDLQRLLE
Pdglb MNRCWA.LFL SLCCYLRVS AEGDPIPEEL YEMLSDEIR SFDDLQRLLE
VegfMNFIL SWHWSLALL LY.....
Vegf2MTV LYPEYWKMKY CQ.....

51

100

Pdgfa IDSVGSEDSL DTSIRAHGVH ATKHVPEKRP LPIRRKRSI.EEAVP
Pdglb GDP.GEEDGA ELDLNMTRSH SGCELES... .LARGRRSLG SLTIAEPAMI
Vegf APMAE..... .GGGQ NHHEVVKFMD .VYQR.....
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....

101

150

Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIMPBC VEVKRCCTGCC NTSVVKCQPS
Pdglb AECRTREVF EISRLIDRT NANFLVMPBC VEVQRCSGCC NNRNVQCRPT
Vegf SYCHPIETLV DIFQYRDEI ..EYIFKPSV VPLMRCGGCC NDEGLECVPT
Vegf2 TCCMPREVCV DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCVNT

151

200

Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.....AT.....
Pdglb QVQLRPQVR KIEIVRKKPI FKKAATVTLLEO HIAKCK.....ETVAAARPVT
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLO HNKCECRPKK DRARQEKKSIV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

FIG. 3A

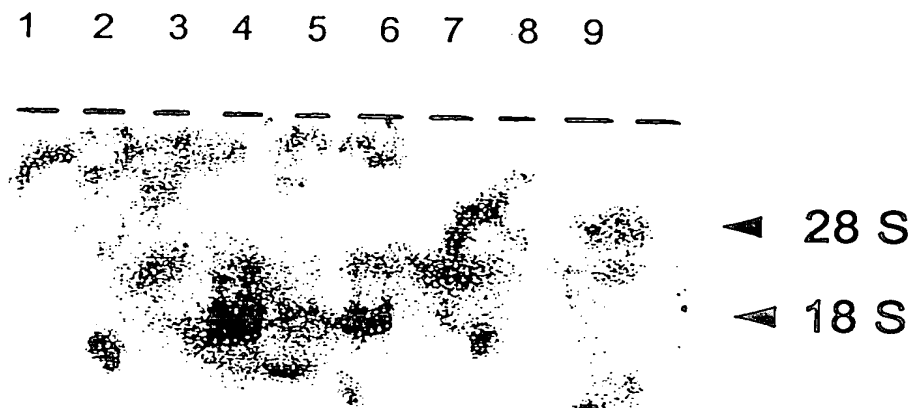
FIG. 3A is a schematic diagram of a protein structure. The diagram shows a sequence of amino acids represented by single-letter codes. The sequence is divided into four segments: Pdgfa, Pdglb, Vegf, and Vegf2. The Pdgfa segment is 101 residues long, Pdglb is 150 residues long, Vegf is 151 residues long, and Vegf2 is 200 residues long. The sequence is shown in a linear fashion, with the first residue on the left and the last residue on the right. The sequence is: Pdgfa: .MRTIACLLL LGGCYLAHVL AEEAEIPREV IERLARSQH SIRDLQRLLE; Pdglb: MNRCWA.LFL SLCCYLRVS AEGDPIPEEL YEMLSDEIR SFDDLQRLLE; Vegf:MNFIL SWHWSLALL LY.....; Vegf2:MTV LYPEYWKMKY CQ.....

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN
EACH PAIR OF GENES IS SHOWN IN THE
FOLLOWING TABLE

	PDGF α	PDGF β	VEGF	VEGF2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

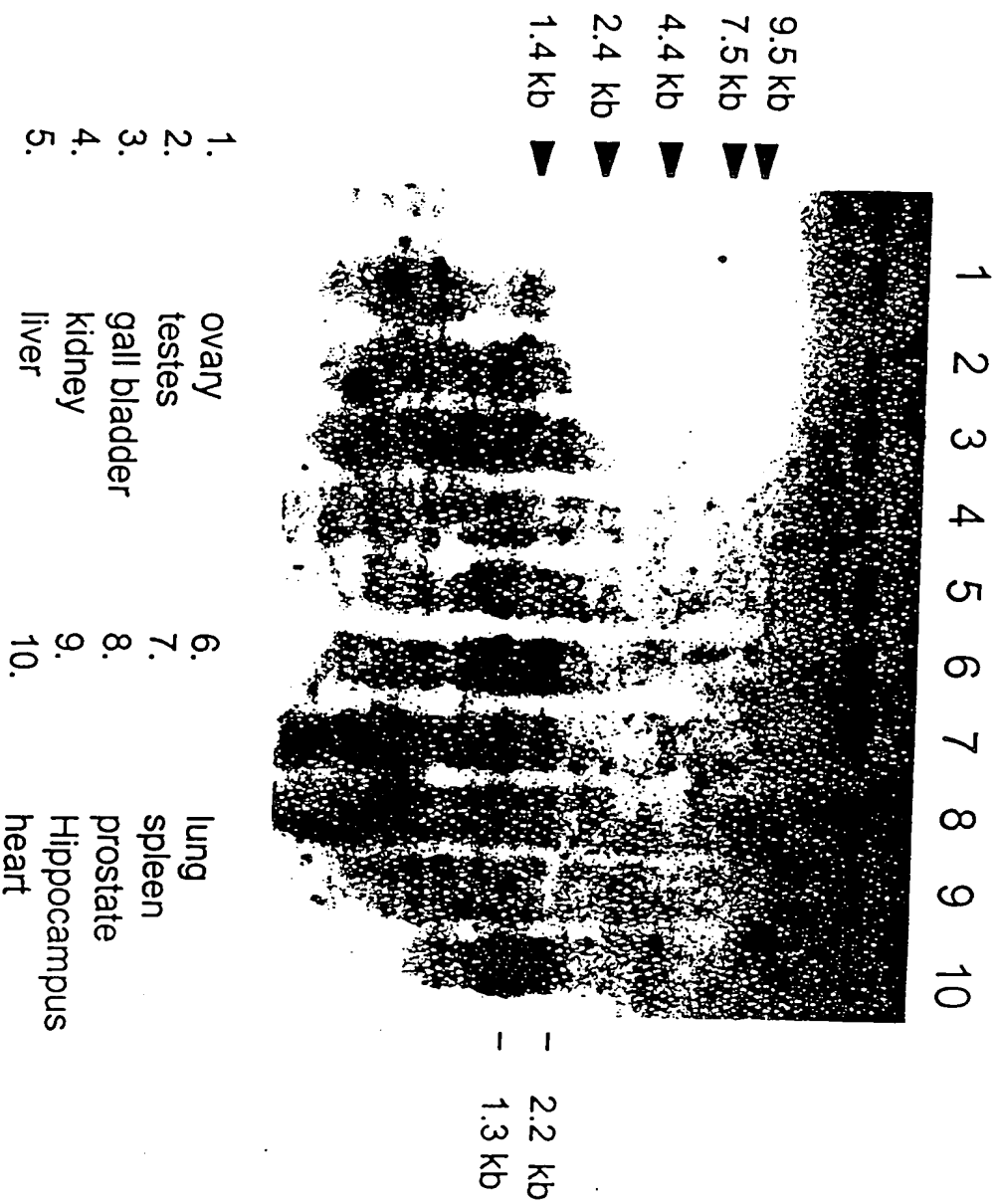
FIG. 4

Expression of VEGF2 mRNA in
Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
- 3-9. breast tumor cell lines.

FIG. 5

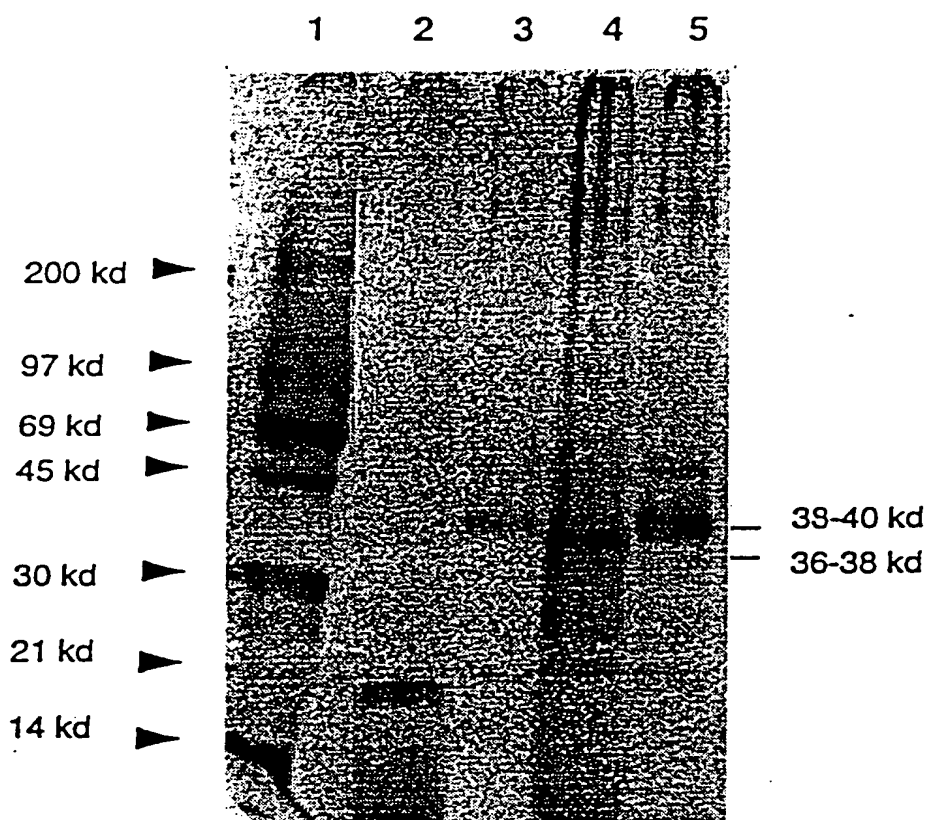


Expression of VEGF2 mRNA in human adult tissues.

FIG. 6

FIG. 6 shows the expression of VEGF2 mRNA in human adult tissues. The tissues are: 1. ovary, 2. testes, 3. gall bladder, 4. kidney, 5. liver, 6. lung, 7. spleen, 8. prostate, 9. Hippocampus, and 10. heart. The molecular weight markers are indicated on the left and right sides of the blot.

FIG. 7



- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primers)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG. 9

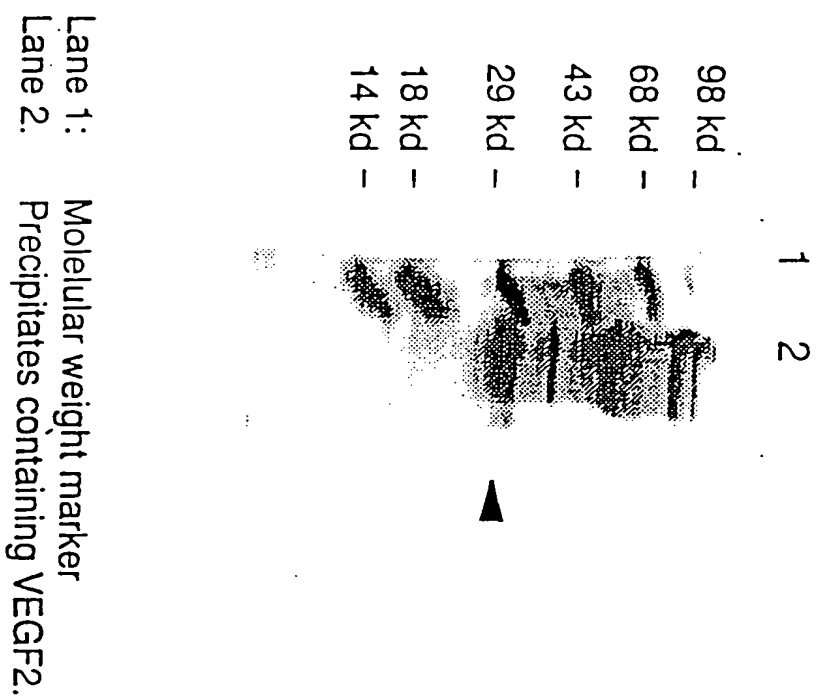


FIG. 10

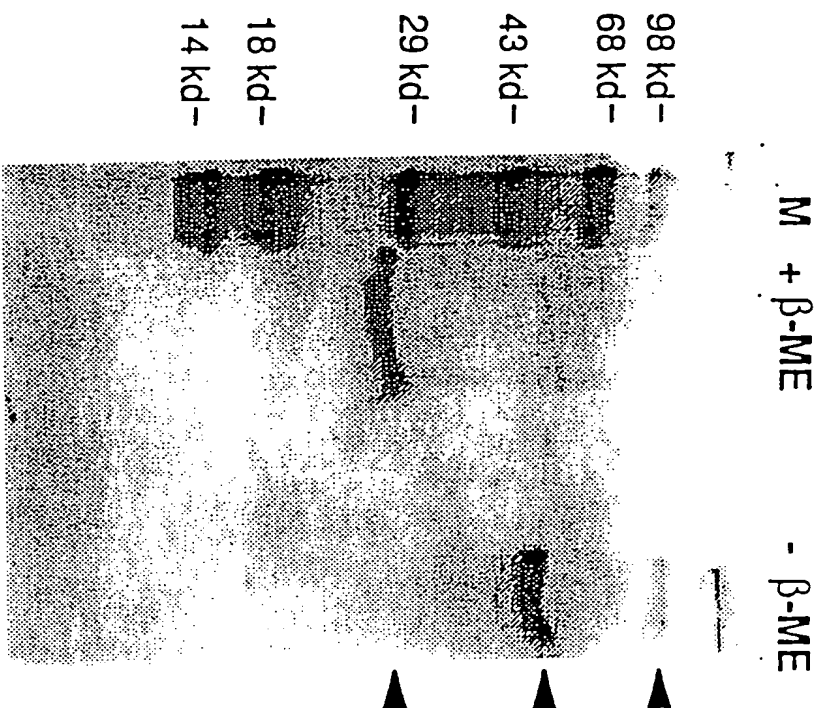


FIG. 11

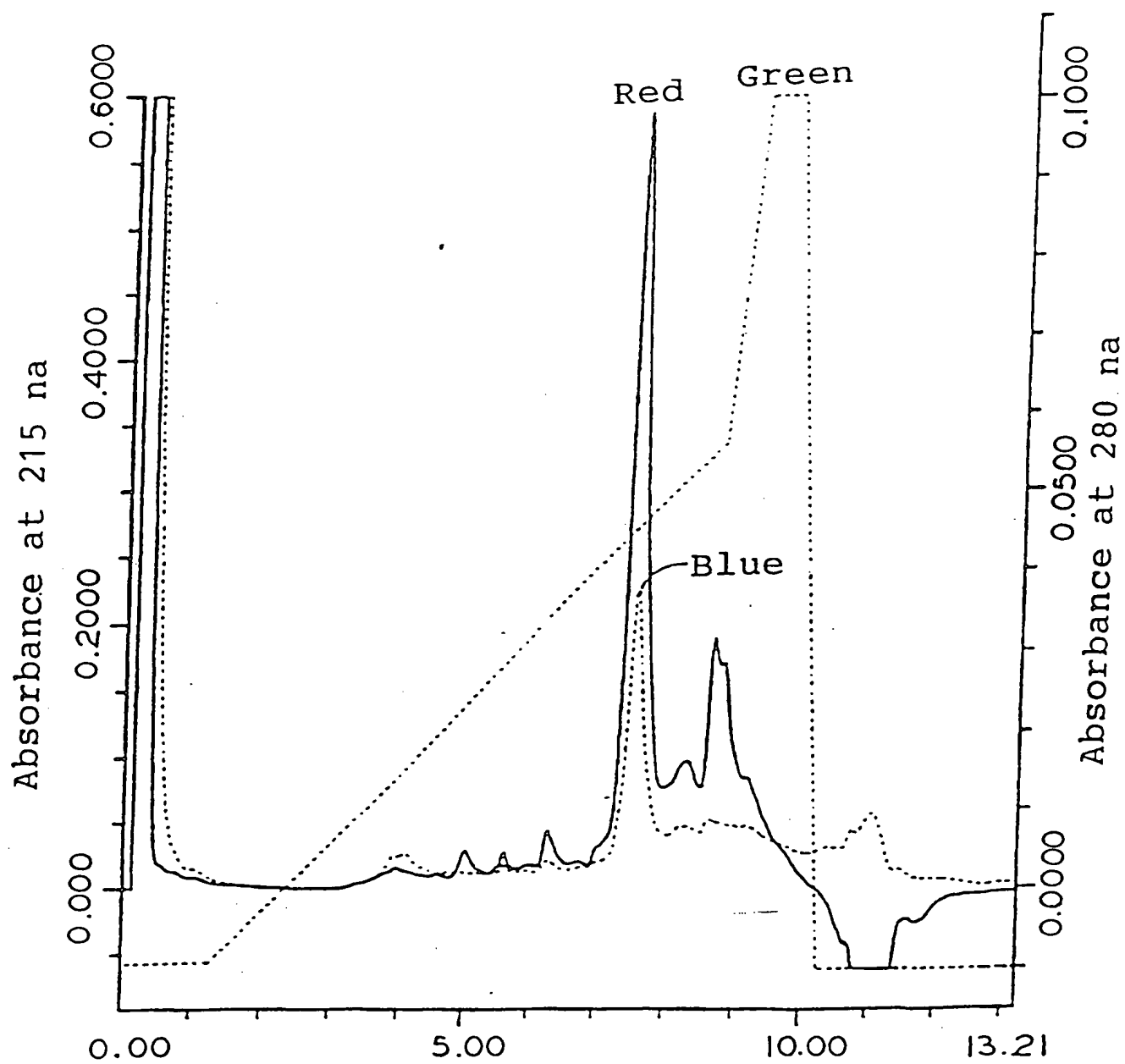


FIG. 12

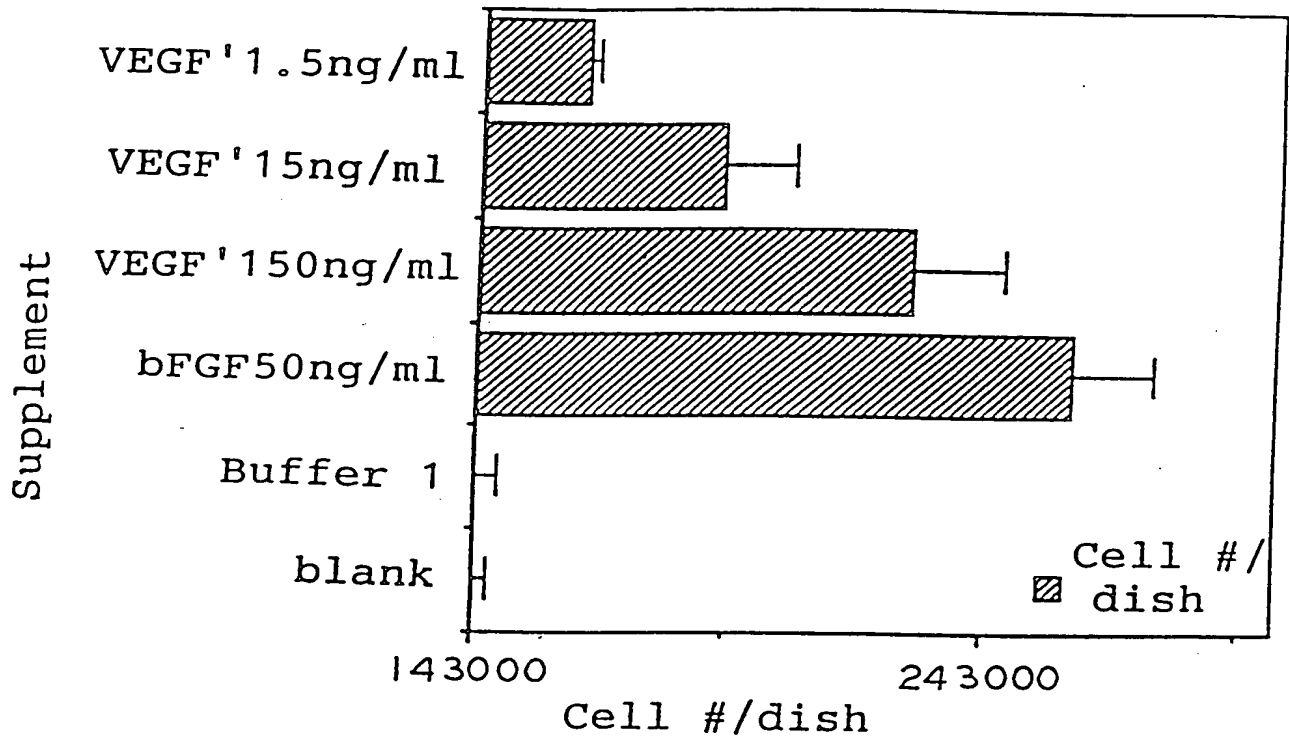


FIG. 13

